acids and contain in each case 10 to 80 consecutive nucleotides from

(i) the same highly conserved region of the LTR region, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 1 to 13,

(ii) a corresponding region of another HI virus isolate,

(iii) a corresponding region of a consensus sequence derived from several HI virus isolates or sequences which are complementary thereto, and

(b) carrying out an enzymatic amplification step.

2. (Amended) The method [Method] as claimed in claim 1, further comprising [wherein it comprises] the steps:

(a) contacting the [a] sample with the oligonucleotides under such conditions that the oligonucleotides hybridize with the HIV nucleic acids from HIV-1 or/and HIV-2 that are present in the sample, and

(b) determining the presence and/or the amount of HIV nucleic acids in the sample.

3. (Amended) The method [Method] as claimed in claim 1 [or 2], wherein only a single oligonucleotide combination is used.

4. (Amended) The method [Method] as claimed in claim 1 [one of the claims 1 to 3], wherein the oligonucleotides are selected for a subtype-independent detection in such a manner that at least 7 of the HIV-1 subtypes selected from the subtypes A, B, C, D, E, F, G, H and O and at least 2 of the HIV-2 subtypes selected from the subtypes A, B, C and D are detected.

5. (Amended) The method [Method] as claimed in claim 1 [one of the claims 1 to 3], wherein the oligonucleotides are selected for a species-independent detection in such a manner that at least 7 of the HIV-1 subtypes selected from the subtypes A, B, C, D, E, F, G, H and O and additionally at least one of the HIV-2 subtypes selected from the subtypes A, B, C and D are detected.

6. (Amended) A method [Method] for the subtype-independent [and/]or species-independent detection of nucleic acids of HI viruses in a sample comprising [by]

(a) hybridizing the nucleic acids with two or more oligonucleotide combinations, each oligonucleotide combination comprising a first oligonucleotide which comprises

10 to 80 consecutive nucleotides from

(i) a highly conserved region of the LTR region, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 1 to 13,

(ii) a corresponding region of another HI virus isolate,

(iii) a corresponding region of a consensus sequence derived from several HI virus isolates, or sequences which are complementary thereto, and a second oligonucleotide which enables subtype-specific [and/]or species-specific hybridization with HIV nucleic acids, and

(b) carrying out an enzymatic amplification step, wherein the entirety of the oligonucleotide combinations allows a subtype-independent [and/]or species-independent detection of HI viruses.

7. (Amended) The method [Method] as claimed in claim 6, wherein the oligonucleotides are selected for the subtype-independent detection in such a manner that at least 7 of the HIV-1 subtypes selected from the subtypes A, B, C, D, E, F, G, H and O and at least 2 of the HIV-2 subtypes selected from the subtypes A, B, C and D are detected.

8. (Amended) The method [Method] as claimed in claim 7, wherein at least two oligonucleotides are used for the detection which contain in each case 10 to 80 consecutive nucleotides from

(i) a highly conserved region of the LTR gene, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 2, 4, 5, 6, 8, 9, 10, 12 and 13,

(ii) a corresponding region of another HI virus isolate,

(iii) a corresponding region of a consensus sequence derived from several HI virus isolates or sequences which are complementary thereto.

9. (Amended) The method [Method] as claimed in claim 6, wherein the oligonucleotides are selected for the species-independent detection in such a manner that at least 7 of the HIV-1 subtypes selected from the subtypes A, B, C, D, E, F, G, H and O and additionally at least one of the HIV-2 subtypes selected from the subtypes A, B, C and D are detected.

10. (Amended) The method [Method] as claimed in claim 9, wherein at least two oligonucleotides are used for the detection which contain in each case 10 to 80 consecutive nucleotides from
(i) a highly conserved region of the LTR gene, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 1, 2, 3, 4, 5, 7, 9, 10 and 13,
(ii) a corresponding region of another HI virus isolate,
(iii) a corresponding region of a consensus sequence derived from several HI virus isolates or sequences which are complementary thereto.

11. (Amended) The method of claim 1, [Method as claimed in one of the previous claims,] wherein the oligonucleotides have or contain the sequences shown in SEQ ID NO. 14 to 25.

12. (Amended) The method of claim 1, [Method as claimed in one of the previous claims,] wherein at least one oligonucleotide has one or several labels.

13. (Amended) An oligonucleotide comprising [Oligonucleotide, wherein it comprises] 10 to 80 consecutive nucleotides from
(i) a highly conserved region of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 4, 5, 9 or 10,
(ii) a corresponding region of another HI virus isolate,
(iii) a corresponding region of a consensus sequence derived from several HI virus isolates or sequences which are complementary thereto, provided that it does not comprise the nucleotide sequence
CTACTACTCC TTGACTTTGG GGATTG
or its complementary sequence.

14. (Amended) The oligonucleotide [Oligonucleotide] as claimed in claim 13, [wherein it comprises] comprising 10 to 80 consecutive nucleotides from
(i) a highly conserved region of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 4, 5 or 9,
(ii) a corresponding region of another HI virus isolate,
(iii) a corresponding region of a consensus sequence derived from several HI virus isolates or sequences which are complementary thereto.

15. (Amended) An oligonucleotide comprising [Oligonucleotide, wherein it comprises at least] one of the sequences shown in SEQ ID NO. 14, 16, 17, 18, 20, 22, 23, 24 and 25.

16. (Amended) The oligonucleotide of claim 13 or 15 [Oligonucleotide as claimed in one of the claims 13 to 15,] wherein it has no mismatches at its 3' end with nucleic acids of the subtypes A, B, C, D, E, F, G, H and O of HIV-1 and of the subtypes A, B, C and D of HIV-2.

17. (Amended) The oligonucleotide of claim 13 or 15 [Oligonucleotide as claimed in one of the claims 13 to 16,] wherein it has one or several labels.

18. (Amended) An oligonucleotide combination [Combination of several oligonucleotides] comprising at least two oligonucleotides, wherein [the at least two oligonucleotides] each oligonucleotide comprises [comprise] 10 to 80 consecutive nucleotides from

(i) a highly conserved region of the LTR region, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 1 to 13,

(ii) a corresponding region of another HI virus isolate,

(iii) a corresponding region of a consensus sequence derived from several HI virus isolates or sequences which are complementary thereto and the combination is selected such that it allows an enzymatic amplification.

19. (Amended) An oligonucleotide combination [Combination of several oligonucleotides] comprising at least two oligonucleotides selected from the oligonucleotides as claimed in claim 13 or 15 [one of the claims 13 to 17] and optionally additional oligonucleotides each of which contains [which each contain] a sequence that is specific for a single subtype of HIV-1 and/or HIV-2, wherein the entirety of the oligonucleotides allows a subtype-independent and/or species-independent detection of HI viruses.

20. (Amended) A [Reagent] kit comprising an oligonucleotide as claimed in claim 13 or 15 [one of the claims 13 to 17 or an oligonucleotide combination as claimed in claim 18 or 19] as primers and/or probes for the detection of HI viruses or their nucleic

acids and suitable means for carrying out a hybridization and amplification of nucleic acids in a sample.

21. (Amended) A method of using [Use of] oligonucleotides [or oligonucleotide combinations] as claimed in claim 13 or 15 [one of the claims 13 to 19] as primers and/or probes for the subtype-independent and/or species-independent detection of HI viruses.

REMARKS

Applicants have amended the claims to comply with U.S. patent practice in matters of form and to remove certain multiple dependency. After entry of this Amendment, claims 1-21 are pending in this application. The amendments do not introduce new matter. Entry of this Amendment is respectfully requested.

The total filing fee on the Transmittal Letter To The United States Designated/Elected Office (DO/EO/US) Concerning A Filing Under 35 U.S.C. §371 is calculated on the basis of this Amendment.

Respectfully submitted

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